SARS-CoV-2 Sequencing and Variants in Washington State

Washington State Department of Health

November 16, 2022

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Next Generation Sequencing (NGS) is a set of laboratory methods that scientists use to scan a viral genome to determine the genome sequence of a virus. A genome sequence of a virus is referred to as its "genomic fingerprint," and can reveal mutations in a virus that make it unique. Mutations are changes in a genome sequence and occur naturally over time.

Scientists compare viral genomes to better understand how viruses can spread from person to person. NGS technology allows public health officials to detect clusters of cases and monitor new variant viruses. Groups of same-species viruses that share a set of genome mutations are referred to as a lineage. Some variants belonging to specific lineages may have characteristics such as the ability to spread more quickly, cause more severe disease, or impact clinical therapy such as treatment with monoclonal antibodies. These variants may be classified as variants of interest, variants being monitored, variants of concern or variants of high concern.

Throughout this report, we refer to the scientific name of the virus SARS-CoV-2 that causes COVID-19. Sequencing can only be performed on samples that are processed in laboratories and where swabs are stored in liquid that is compatible with sequencing, which means only samples used for molecular tests (such as PCR) can be included. For this reason, this report is limited to confirmed cases only. The genomes that are sequenced and compared are those of the virus, not of humans.

At a glance (data through November 15, 2022)

- During the month of October 2022, **14.2%** of all confirmed molecular COVID-19 cases were sequenced. This number is preliminary and will change over time as additional specimens are received from the previous month.

- **127,920 (9.6%)** COVID-19 cases in Washington state have sequencing information available since January 2021.

CDC currently categorizes variants as Variants of High Consequence (VOHC), Variants of Concern (VOC), Variants of Interest (VOI) and Variants Being Monitored (VBM). There are currently no VOHC and VOI so only VOC and VBM are detailed in this report.

Variants of Concern

Variant	Area first detected	Background	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Omicron (B.1.1.529, BA.1, BA.1.1, BA.2, BA.3, BA.4 and BA.5 lineages)	South Africa	Early research indicates evidence for increased transmissibility, immune evasion, and lower risk of hospitalization and death, relative to Delta. Approved vaccines are effective at preventing severe disease and death against Omicron variants	62,001	Nov 29, 21	Nov 02, 22

*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

Note: Omicron lineages in this report are defined as below:

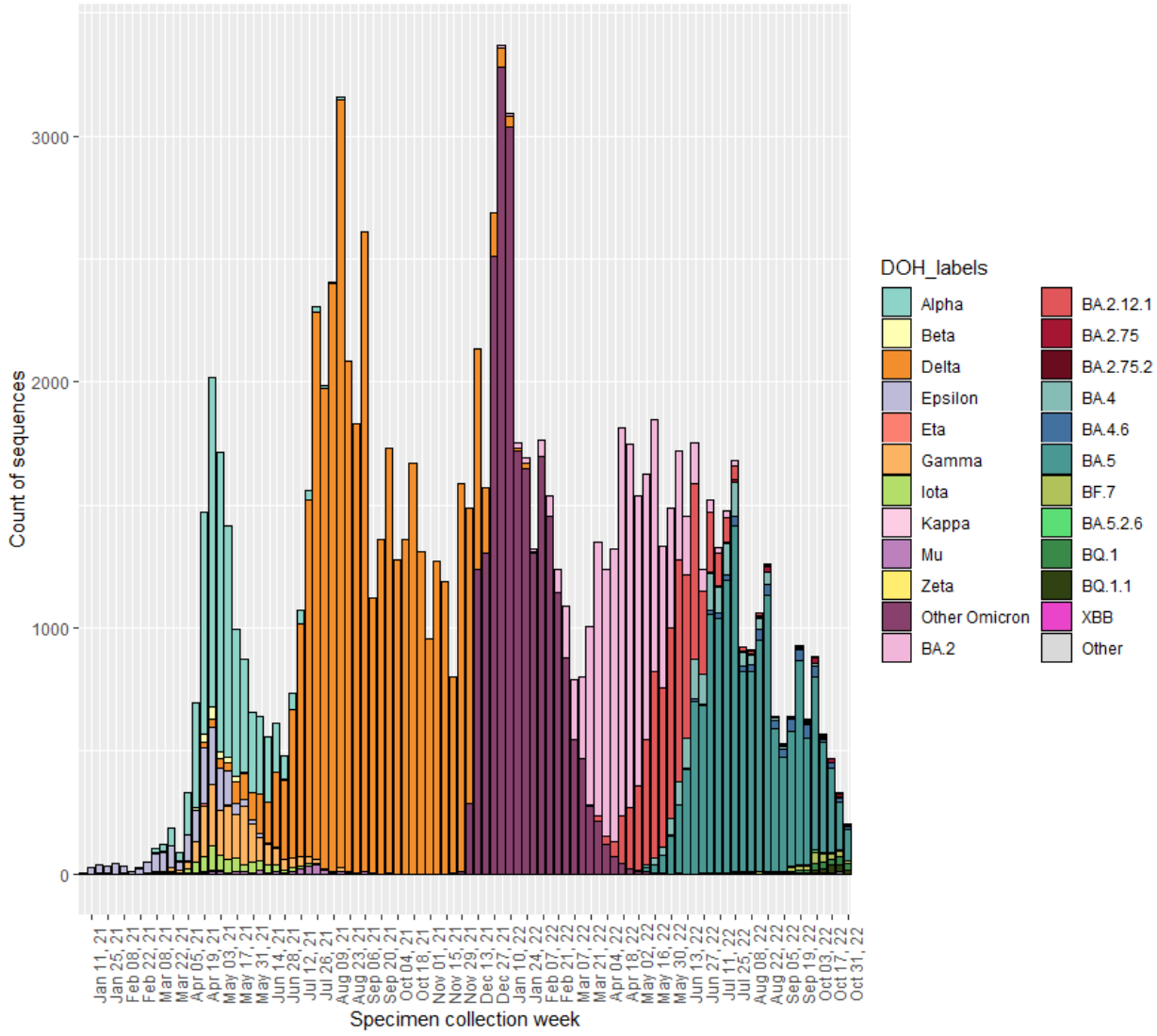
Omicron grouping	Inclusion
Other Omicron	Includes B.1.1.529, BA.1.X, BA.3.X
BA.2	Includes BA.2.X except BA.2.12.1 and BA.2.75.X
BA.2.12.1	Includes BA.2.12.1.X
BA.2.75	Includes BA.2.75.X except BA.2.75.2
BA.2.75.2	Includes BA.2.75.2.X
BA.4	Includes BA.4.X except BA.4.6.X
BA.4.6	Includes BA.4.6.X
BA.5	Includes BA.5.X except BF.7 and BA.5.2.6
BA.5.2.6	Includes BA.5.2.6.X
BF.7	Includes BF.7.X (Alias of B.1.1.529.5.2.1.7)
BQ.1	Includes BQ.1 (Alias of BA.5.3.1.1.1.1.1) except BQ.1.1
BQ.1.1	Includes BQ.1.1.X

Variants Being Monitored

Variant	Area first detected	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Alpha (B.1.1.7)	United Kingdom	10,344	Jan 07, 21	Sep 08, 21
Beta (B.1.351)	South Africa	282	Jan 29, 21	Jun 29, 21
Delta (B.1.617.2 and AY lineages)	India	38,972	Apr 03, 21	Sep 02, 22
Epsilon (B.1.427 / B.1.429)	California	4,205	Dec 11, 20	Jun 24, 21
Eta (B.1.525)	New York	92	Feb 02, 21	Jun 08, 21
Gamma (P.1)	Brazil	2,499	Feb 06, 21	Dec 02, 21
Iota (B.1.526)	New York	935	Jan 21, 21	Aug 20, 21
Kappa (B.1.617.1)	India	46	Mar 22, 21	Jun 14, 21
Mu (B.1.621)	Colombia	219	Apr 09, 21	Dec 20, 21
Zeta (P.2)	Brazil	45	Jan 18, 21	Apr 20, 21

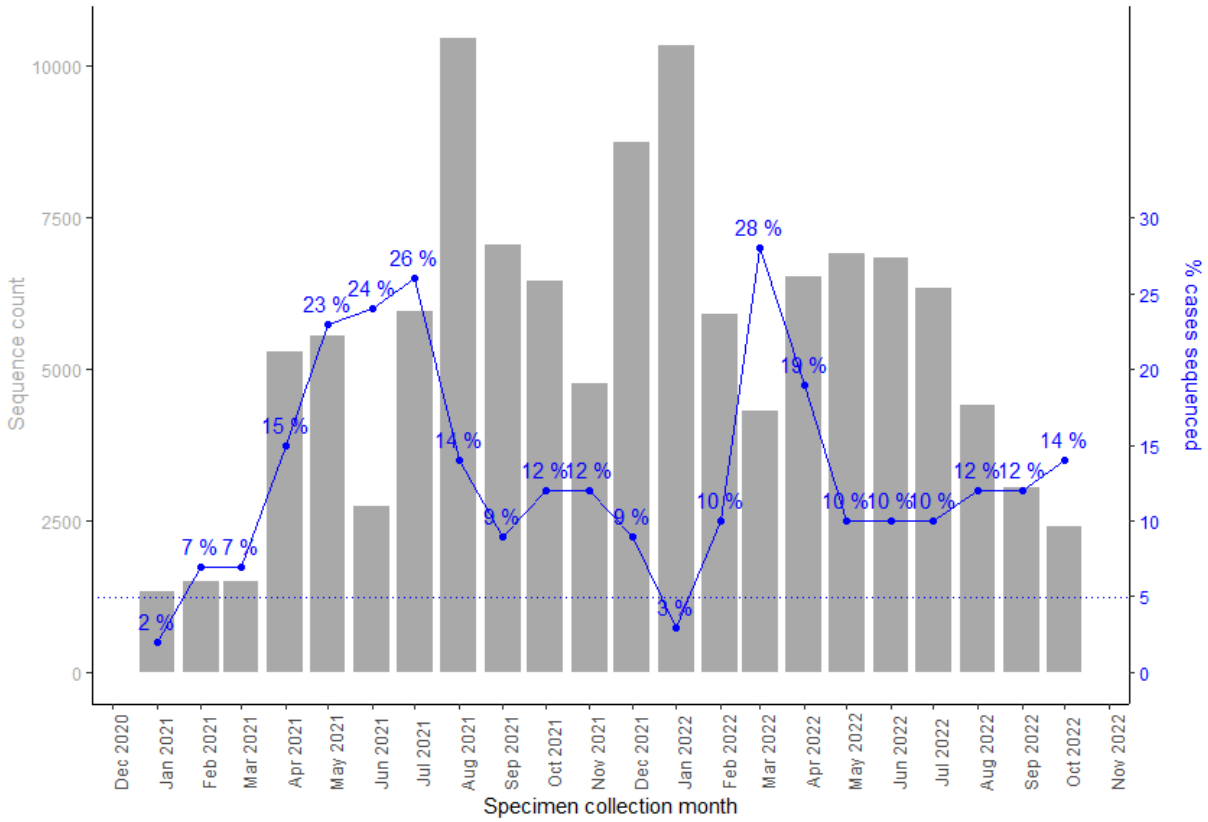
*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

Epidemiologic curve of variants being monitored and variants of concern by week of specimen collection date from January 01, 2021 to November 04, 2022



- The above graph shows the total number of variants detected by the week the specimen was collected from a patient.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.
- This graph shows all specimens sequenced, including specimens sequenced during outbreaks and other targeted sequencing efforts.
- “Other Omicron “ includes B.1.1.529, BA.1 and BA.3 sublineages

Number of specimens sequenced, and percent of Washington State confirmed COVID-19 cases that have been sequenced by specimen collection date from January 2021 through October 2022.

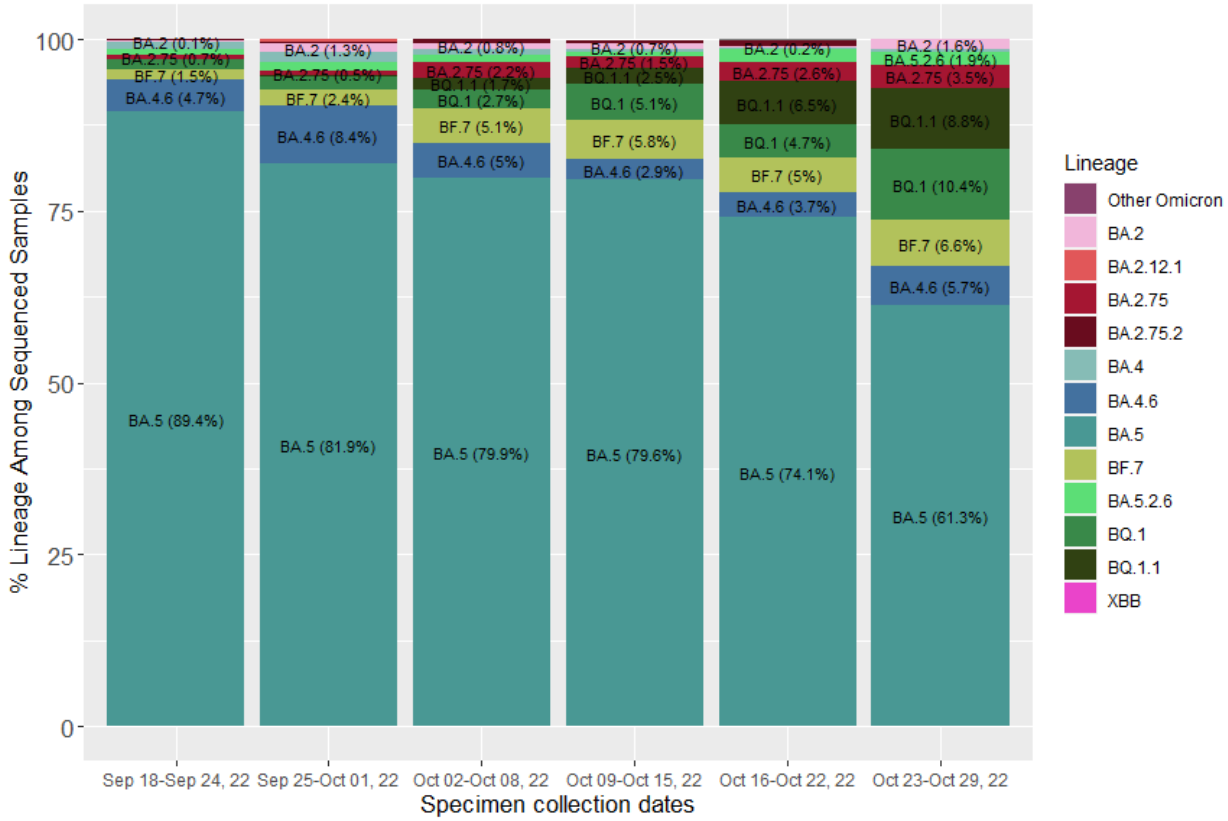


- Samples are not sequenced for every confirmed COVID-19 case. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing can be performed on stored specimens at any time, so numbers from past months may change if stored specimens are sequenced.

SARS-CoV-2 Lineages Circulating in Washington State

The graph below shows the change in proportion of select SARS-CoV-2 lineages by time period. A viral lineage is a group of viruses that descend from a common ancestor with shared genetic characteristics, allowing them to be grouped together. As the proportions of variants increase, the proportion of other lineages will decrease.

NOTE: The data on this graph come from cases that are randomly selected for sequencing statewide, Cases sequenced because they were part of an outbreak or were otherwise manually selected for sequencing are excluded.



The chart above shows the proportions of the most common SARS-CoV-2 lineages circulating in Washington grouped in one-week intervals. Proportions are calculated using data which are subject to change over time and will be updated as more data becomes available, including data from prior time periods. **Due to the time it takes to complete sequencing, the most recent time period is based on a very small number of sequences and likely to be adjusted over time.**

To see the national trends, visit the CDC's variant proportions page.

The table below shows the current number of variants of concern (VOC) detected by county of home address since January 2022; data is from the Washington Disease Reporting System (WDRS).

	VOC													
County	Other Omicron	BA.2	BA.2.12.1	BA.2.75	BA.2.75.2	BA.4	BA.4.6	BA.5	BF.7	BA.5.2.6	BQ.1	BQ.1.1	XBB	Total current VOC specimens sequenced
Adams	270	3	6	0	0	0	0	15	0	0	0	0	0	90
Asotin	90	1	4	0	0	2	0	9	0	0	0	0	0	30
Benton	3,232	102	98	0	1	20	7	290	2	0	1	0	0	1,078
Chelan	1,788	61	95	0	0	22	6	233	3	1	0	2	0	597
Clallam	1,976	175	61	0	0	22	8	181	4	0	0	0	0	660
Clark	3,584	300	195	0	1	36	7	292	4	0	2	2	0	1,196
Columbia	24	1	1	0	0	0	0	0	0	0	0	0	0	8
Cowlitz	1,802	87	66	0	0	8	0	116	1	0	0	0	0	601
Douglas	1,008	45	40	0	0	5	0	132	0	0	0	0	0	336
Ferry	45	2	3	0	0	0	0	0	0	0	0	0	0	15
Franklin	2,880	38	39	0	2	25	3	359	3	2	1	0	0	961
Garfield	9	1	1	0	0	0	0	1	0	0	0	0	0	3
Grant	1,185	26	32	0	0	6	0	65	0	0	0	0	0	395
Grays Harbor	2,131	97	51	0	0	9	24	126	2	0	0	0	0	711
Island	921	119	42	0	0	8	6	60	0	0	0	0	0	307
Jefferson	312	12	7	0	0	0	0	17	0	0	0	0	0	104
King	81,591	7,655	3,313	96	18	719	295	7,942	144	37	132	92	20	27,245
Kitsap	2,890	228	121	2	0	25	11	298	2	0	0	0	0	964
Kittitas	300	17	5	0	0	2	0	8	0	0	0	0	0	100
Klickitat	105	7	3	0	0	0	0	7	0	0	0	0	0	35
Lewis	1,065	24	23	0	0	4	4	50	0	0	0	0	0	355
Lincoln	87	4	0	0	0	1	0	18	0	0	0	0	0	29
Mason	1,041	36	23	0	0	5	9	154	0	3	0	0	0	347
Okanogan	630	15	34	0	0	0	4	13	0	0	0	0	0	210

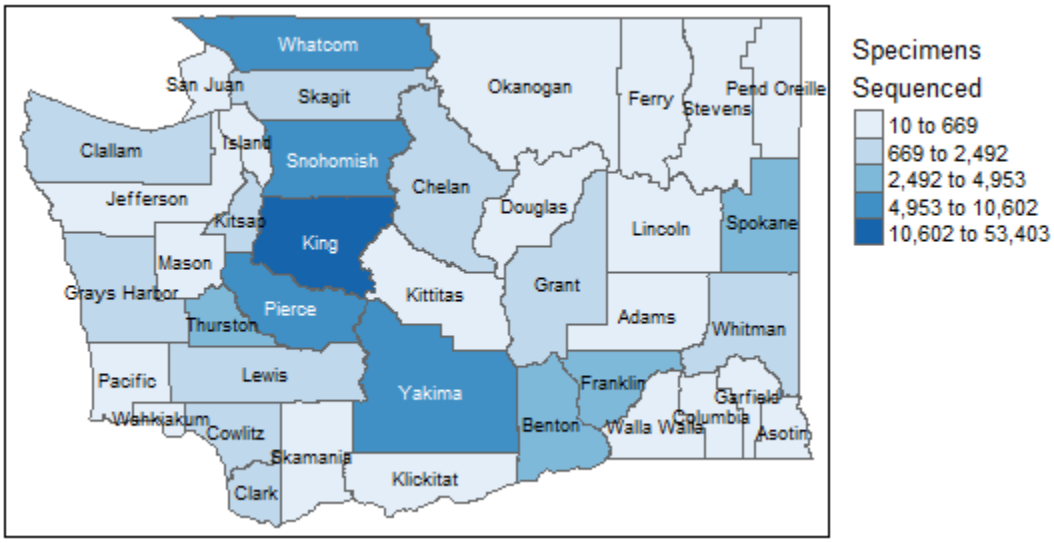
	VOC													
County	Other Omicron	BA.2	BA.2.12.1	BA.2.75	BA.2.75.2	BA.4	BA.4.6	BA.5	BF.7	BA.5.2.6	BQ.1	BQ.1.1	XBB	Total current VOC specimens sequenced
Pacific	486	13	22	0	0	3	0	13	0	0	0	0	0	162
Pend Oreille	60	2	2	0	0	0	0	3	0	0	0	0	0	20
Pierce	11,127	802	492	0	0	97	34	965	12	5	7	4	0	3,713
San Juan	75	5	3	0	0	0	0	1	0	0	0	0	0	25
Skagit	3,160	314	135	3	0	48	11	372	2	0	1	1	0	1,054
Skamania	44	0	3	0	0	0	0	5	1	0	0	0	0	15
Snohomish	15,174	1,457	703	16	9	118	59	1,492	18	9	12	4	0	5,064
Spokane	4,085	173	139	0	0	35	11	287	1	2	0	0	0	1,362
Stevens	135	4	2	0	0	0	0	12	0	0	0	0	0	45
Thurston	6,181	263	165	0	0	22	11	337	2	1	1	0	0	2,061
Wahkiakum	48	6	2	0	0	1	0	0	0	0	0	0	0	16
Walla Walla	942	27	64	0	0	3	12	36	0	0	1	0	0	314
Whatcom	11,087	1,294	648	4	0	122	33	945	7	5	2	1	0	3,698
Whitman	954	58	25	0	0	2	1	45	0	0	0	0	0	318
Yakima	6,361	131	116	1	0	51	8	472	2	0	1	0	0	2,121

- In this table, “Other Omicron” includes all B.1.1.529, BA.1, and BA.3 sublineages

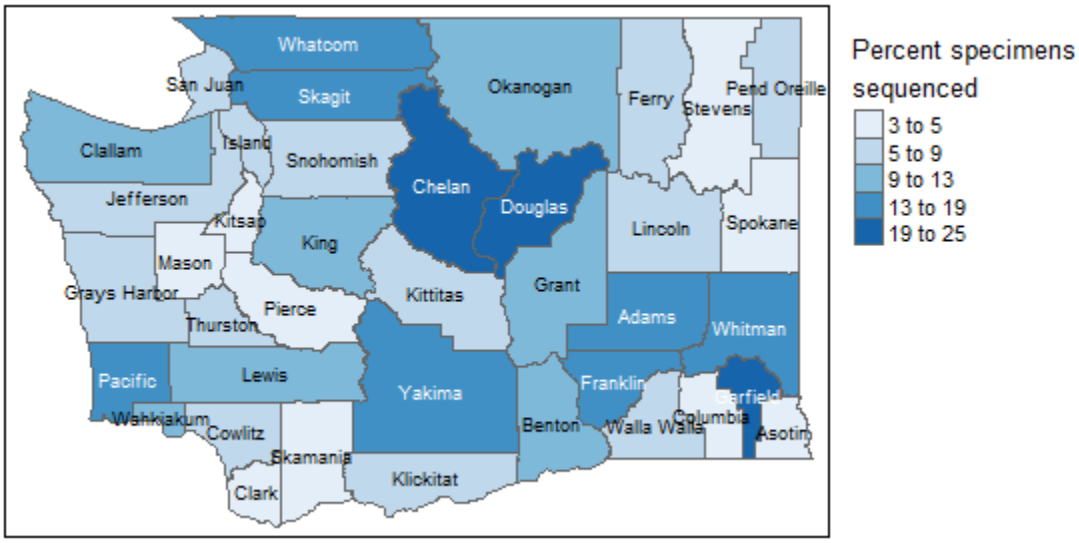
Geographic Coverage of Sequencing

Efforts are made to sequence specimens from all geographic areas of Washington State. The number of sequences and the percent of cases sequenced vary based on several factors including number of cases in that region and which laboratories conduct the majority of testing in each locality.

The map below shows the number of specimens sequenced by county of home address since January 1, 2021.



The map below shows the percent of COVID-19 cases with at least one specimen sequenced by county of home address since January 1, 2021.



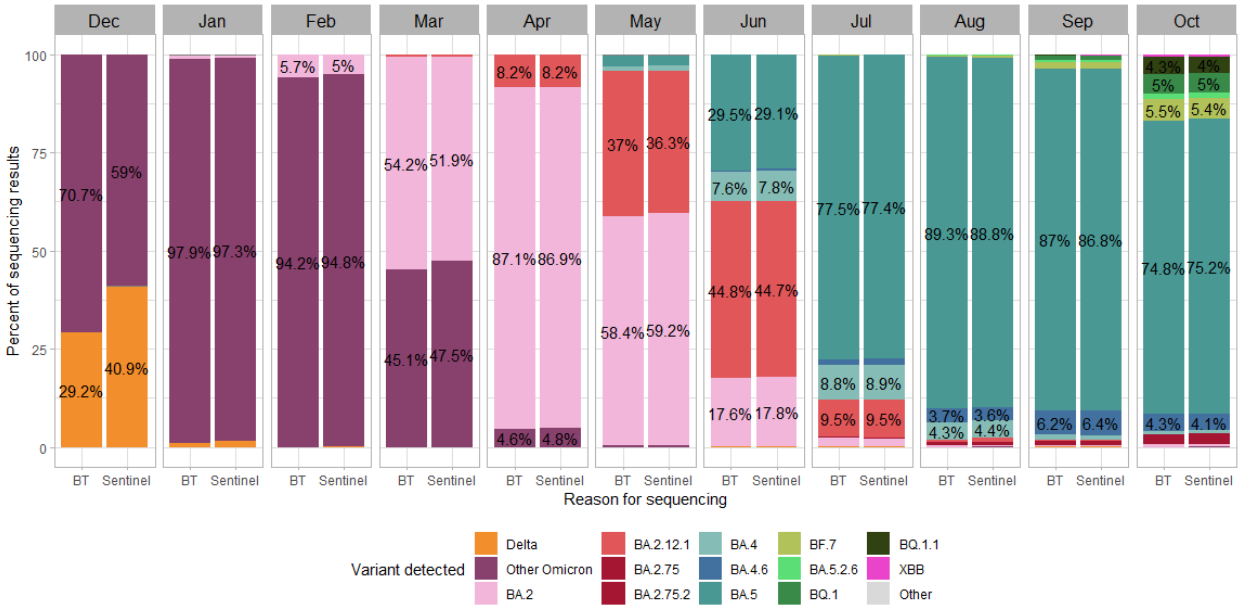
Vaccine Breakthrough Cases

A complete report on vaccine breakthrough cases can be found in the reports section of the DOH data dashboard.

A vaccine breakthrough case is defined as someone who tests positive for SARS-CoV-2 (either a PCR test or antigen test) at least 14 days after a person received their last recommended dose of an authorized, age-appropriate COVID-19 vaccine. DOH is monitoring sequencing results for vaccine breakthrough cases. This can help scientists determine whether any specific variants of the virus are causing more breakthrough cases than expected.

The table and chart below show vaccine breakthrough cases based on lineages. Lineages not designated as VOC, VOI or VBM are marked as 'other'.

Proportion of variants identified among vaccine breakthrough cases (Breakthrough) with sequencing results compared to variants identified among randomly selected COVID-19 cases (Sentinel) during the same time frame. This shows if breakthrough cases are enriched for particular variant(s) compared to the unbiased sentinel controls.



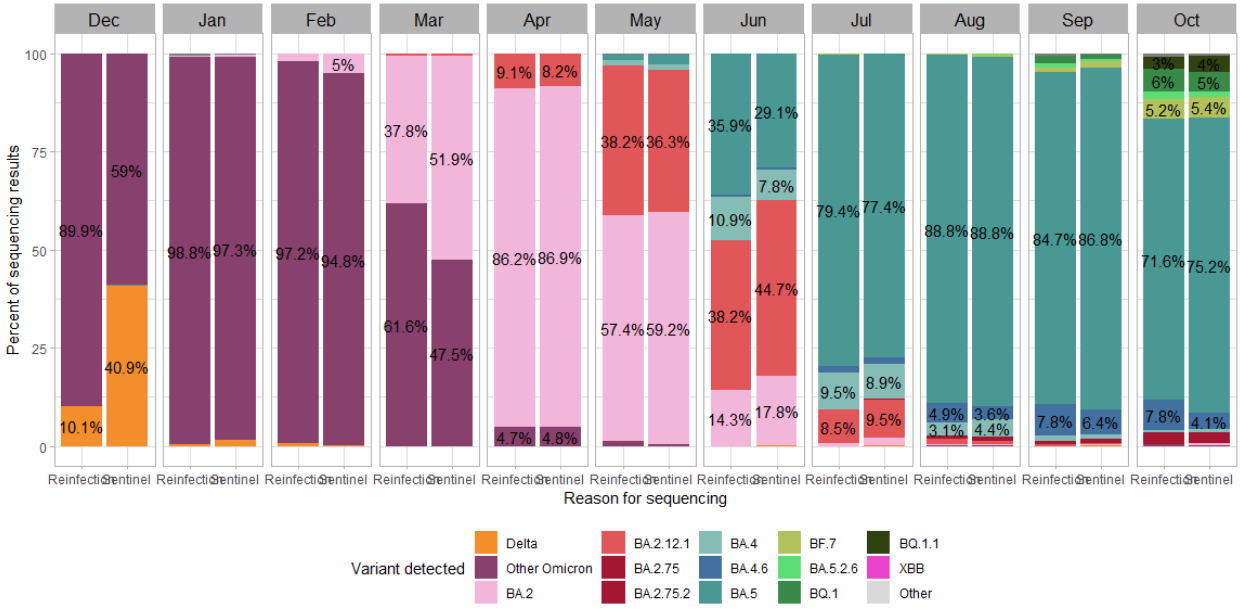
Breakthrough cases by variant table

Variant	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct
Delta	1,473	61	0	0	0	0	1	1	0	1	0
Gamma	1	0	0	0	0	0	0	0	0	0	0
Other Omicron	3,564	6,091	3,576	1,468	231	17	0	0	0	0	0
BA.2	0	42	216	1,764	4,408	3,076	921	103	10	9	14
BA.2.75	0	0	0	0	0	0	1	13	22	18	39
BA.2.75.2	0	0	0	0	0	0	0	0	5	9	9
BA.2.12.1	0	0	0	14	416	1,949	2,345	442	26	7	0
BA.4	0	0	0	0	1	65	397	410	141	27	13
BA.4.6	0	0	0	0	0	0	11	62	120	144	82
BA.5	0	0	0	0	1	140	1,546	3,604	2,933	2,016	1,416
BF.7	0	0	0	0	0	0	0	7	15	37	104
BA.5.2.6	0	0	0	0	0	0	0	1	8	15	27
BQ.1	0	0	0	0	0	0	0	0	0	25	94
BQ.1.1	0	0	0	0	0	0	0	0	0	4	81
XBB	0	0	0	0	0	0	0	0	0	1	13
Other Lineage	6	27	4	7	2	20	11	5	3	4	0

Reinfection

In general, reinfection means a person was infected once with the virus that causes COVID-19, recovered, and then later became infected again. We are still learning about COVID-19 and the duration and strength of immunity following infection with this virus. Based on what we know from similar respiratory viruses, we expect some COVID-19 reinfections to occur. For disease surveillance purposes, a person with a reported reinfection is an individual with two positive COVID-19 test results (molecular or antigen) reported to DOH where the tests were performed at least 90 days apart. In addition, if genetic sequencing of respiratory samples from a patient's first (or primary) infection and most recent infection identifies different variants, they are considered a confirmed reinfection regardless of the amount of time between positive tests. Washington State Department of Health adopted this definition on September 1, 2021.

DOH is monitoring sequencing results for reinfection cases. This can help scientists determine whether any specific variants of the virus are causing more reinfection cases than expected. The table and chart below show reinfection cases based on lineages. Lineages not designated as VOC, VOI or VBM are marked as 'other'. Proportion of variants identified among reinfection cases (Reinfection) with sequencing results compared to variants identified among randomly selected COVID-19 cases (Sentinel) during the same time frame.



Reinfection cases by variant table

Please note - data for the most recent month are incomplete

Variant	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct
Delta	28	2	2	0	0	0	0	0	0	0	0
Other Omicron	248	633	317	114	11	4	0	0	1	0	1
BA.2	0	2	7	70	200	182	63	4	1	0	0
BA.2.12.1	0	0	0	1	21	121	168	53	6	1	0
BA.2.75	0	0	0	0	0	0	0	0	2	3	6
BA.2.75.2	0	0	0	0	0	0	0	0	2	0	1
BA.4	0	0	0	0	0	4	48	59	14	4	1
BA.4.6	0	0	0	0	0	0	3	10	22	23	18
BA.5	0	0	0	0	0	5	158	492	395	250	166
BF.7	0	0	0	0	0	0	0	1	1	3	12
BA.5.2.6	0	0	0	0	0	0	0	0	1	3	4
BQ.1	0	0	0	0	0	0	0	0	0	6	14
BQ.1.1	0	0	0	0	0	0	0	0	0	0	7
Other VOC/VOI	0	0	0	0	0	0	0	0	0	2	2
Other Lineage	0	4	0	0	0	1	0	1	0	0	0

The hospitalization table below includes sequencing data since January 1, 2021 and does not account for factors that can influence hospitalization rates such as age and vaccination status, which may be different across variants. This means that hospitalization rates are not necessarily comparable between variants.

Hospitalizations and deaths by variant

Variant	Cases who were hospitalized	Cases who died from COVID-19	Total cases
Other Omicron	1.4%	0.5%	23,227
BA.2	1.1%	0.2%	13,613
BA.2.12.1	1.7%	0.3%	6,784
BA.2.75	1.6%	0%	122
BA.2.75.2	0%	0%	31
BA.4	1.8%	0.3%	1,421
BA.4.6	2.8%	0.7%	564
BA.5	2%	0.3%	15,372
BF.7	0.5%	0%	210
BQ.1	0%	0%	161
BQ.1.1	0.9%	0%	106
Alpha	3.5%	0.6%	10,314
Beta	7.1%	1.1%	281
Delta	4.3%	1.3%	38,844
Epsilon	2.6%	0.7%	4,148
Gamma	6.9%	1.7%	2,481
Iota	3.2%	1.3%	932
Mu	2.8%	1.8%	218
Other	2.6%	0.8%	5,197

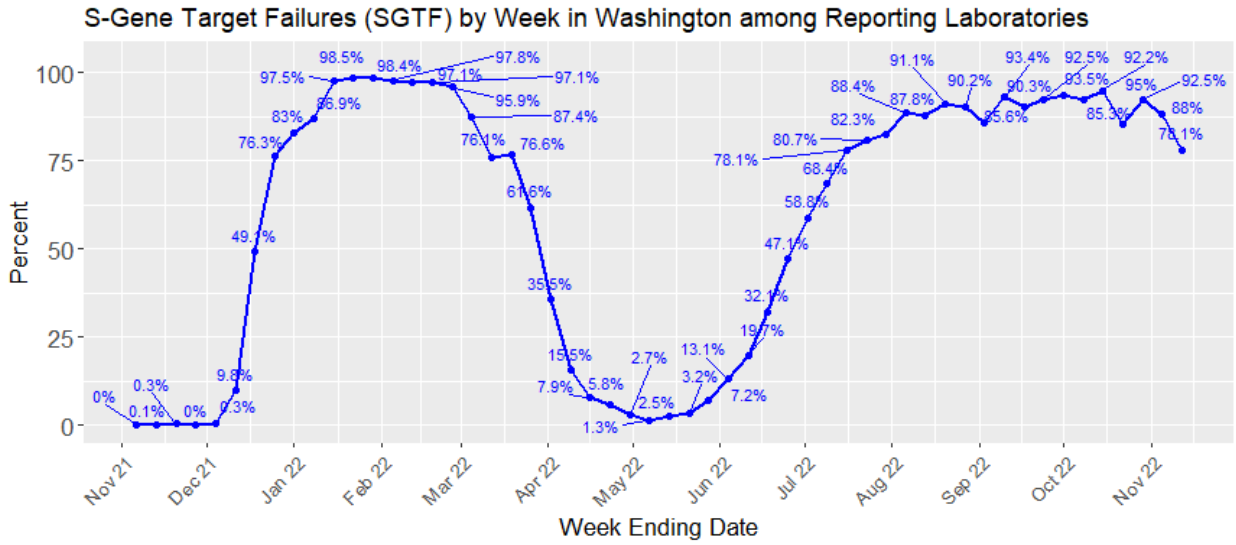
Age distribution by variant

Variant	Age 0-19	Age 20-34	Age 35-49	Age 50-64	Age 65-79	Age 80+	Unknown	Total cases
Other Omicron	24%	32%	21%	13%	5%	2%	2%	23,227
BA.2	19%	32%	23%	14%	7%	2%	2%	13,613
BA.2.12.1	15%	32%	23%	16%	9%	3%	2%	6,784
BA.2.75	11%	22%	31%	20%	11%	1%	4%	122
BA.2.75.2	6%	29%	26%	26%	13%	0%	0%	31
BA.4	17%	31%	25%	15%	7%	2%	3%	1,421
BA.4.6	13%	32%	24%	14%	12%	3%	2%	564
BA.5	12%	29%	24%	18%	11%	3%	3%	15,372
BF.7	9%	26%	24%	21%	12%	5%	2%	210
BQ.1	7%	32%	25%	20%	11%	1%	2%	161
BQ.1.1	12%	25%	23%	22%	10%	6%	3%	106
Alpha	27%	32%	22%	12%	3%	1%	2%	10,314
Beta	29%	34%	21%	12%	3%	0%	1%	281
Delta	23%	29%	22%	14%	7%	2%	2%	38,844
Epsilon	25%	31%	22%	14%	4%	1%	2%	4,148
Gamma	22%	35%	23%	11%	4%	3%	2%	2,481
Iota	25%	33%	24%	12%	4%	1%	1%	932
Mu	22%	37%	22%	10%	6%	1%	2%	218
Other	24%	29%	23%	15%	5%	2%	2%	5,197

*Other includes all variant viruses that are not categorized as VOC or VBM

Tracking Omicron Using Clinical Tests

WA DOH is tracking the Omicron variant using sequencing. One challenge is that the sequencing process can take up to a few weeks, so we use another testing marker known as 'S gene target failure (SGTF)' to identify possible Omicron cases carrying this mutation rapidly and inform public health action; these include BA.1, BA.3, BA.4 and BA.5 and sublineages. BA.2 and BA.2.12.1 do not carry this mutation. While SGTF does not always mean that a case will be finalized as Omicron, greater than 95% of these results are predicted to finalize as Omicron. Many laboratories are sharing this data with WA DOH to help track the spread of Omicron.



A small number of other SARS-CoV-2 viruses other than Omicron can cause SGTF, these can be seen in the small numbers (0-3) seen weekly prior to the week of November 28th. Additionally, the Omicron sub-lineage BA.2 and BA.2.12.1 do not carry this mutation.

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2021-10-31	2021-11-06	1,086	0	0%
2021-11-07	2021-11-13	1,093	1	0.1%
2021-11-14	2021-11-20	1,129	3	0.3%
2021-11-21	2021-11-27	1,267	0	0%
2021-11-28	2021-12-04	2,414	8	0.3%
2021-12-05	2021-12-11	2,342	229	9.8%
2021-12-12	2021-12-18	3,162	1,552	49.1%
2021-12-19	2021-12-25	4,528	3,456	76.3%
2021-12-26	2022-01-01	5,033	4,178	83%
2022-01-02	2022-01-08	10,893	9,469	86.9%
2022-01-09	2022-01-15	13,481	13,149	97.5%
2022-01-16	2022-01-22	11,754	11,581	98.5%
2022-01-23	2022-01-29	8,363	8,233	98.4%
2022-01-30	2022-02-05	4,686	4,581	97.8%
2022-02-06	2022-02-12	2,696	2,619	97.1%
2022-02-13	2022-02-19	1,372	1,332	97.1%
2022-02-20	2022-02-26	627	601	95.9%
2022-02-27	2022-03-05	478	418	87.4%
2022-03-06	2022-03-12	355	270	76.1%
2022-03-13	2022-03-19	334	256	76.6%
2022-03-20	2022-03-26	375	231	61.6%
2022-03-27	2022-04-02	332	118	35.5%
2022-04-03	2022-04-09	381	59	15.5%
2022-04-10	2022-04-16	544	43	7.9%
2022-04-17	2022-04-23	762	44	5.8%
2022-04-24	2022-04-30	1,143	31	2.7%
2022-05-01	2022-05-07	1,190	15	1.3%
2022-05-08	2022-05-14	1,419	36	2.5%
2022-05-15	2022-05-21	1,602	51	3.2%
2022-05-22	2022-05-28	1,516	109	7.2%

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2022-05-29	2022-06-04	1,295	169	13.1%
2022-06-05	2022-06-11	1,270	250	19.7%
2022-06-12	2022-06-18	1,167	375	32.1%
2022-06-19	2022-06-25	1,236	582	47.1%
2022-06-26	2022-07-02	1,092	642	58.8%
2022-07-03	2022-07-09	1,122	767	68.4%
2022-07-10	2022-07-16	999	780	78.1%
2022-07-17	2022-07-23	1,032	833	80.7%
2022-07-24	2022-07-30	979	806	82.3%
2022-07-31	2022-08-06	658	582	88.4%
2022-08-07	2022-08-13	576	506	87.8%
2022-08-14	2022-08-20	551	502	91.1%
2022-08-21	2022-08-27	449	405	90.2%
2022-08-28	2022-09-03	341	292	85.6%
2022-09-04	2022-09-10	271	253	93.4%
2022-09-11	2022-09-17	331	299	90.3%
2022-09-18	2022-09-24	333	308	92.5%
2022-09-25	2022-10-01	429	401	93.5%
2022-10-02	2022-10-08	296	273	92.2%
2022-10-09	2022-10-15	200	190	95%
2022-10-16	2022-10-22	150	128	85.3%
2022-10-23	2022-10-29	160	148	92.5%
2022-10-30	2022-11-05	184	162	88%
2022-11-06	2022-11-12	128	100	78.1%

We thank the reporting laboratories: University of Washington Virology, Avero Diagnostics, The Vancouver Clinic, Atlas Laboratories, Evergreen Health, FidaLab

We gratefully acknowledge the laboratories that tested and sequenced the specimens for reporting the sequencing metadata including the lineages to WA DOH. We also thank the GISAID initiative as the whole genome sequencing data stored in their repository has helped us validate the submissions we receive from laboratories.

The following clinical laboratories have contributed specimens for sequencing:

Aegis Sciences Corporation

Allenmore Hospital Laboratory

Altius Institute for Biomedical Sciences

Atlas Genomics

BioReference Laboratories Inc.

Cascade Valley Hospital

Central Washington Hospital

Coumbia Basin Hospital

Curative Labs Inc.

Dayton General Hospital

Deaconess Hospital

Diatherix Laboratories

Dynacare Northwest Inc.

East Adams Rural Hospital

Everett Clinic Microbiology

Evergreen Healthcare

Ferry County Hospital

FidaLab

Forks Community Hospital

Fulgent Genetics

Gravity Diagnostics, LLC

Harborview Medical Center

Healthquest Esoterics

Helix/Illumina

Incyte Diagnostics Spokane

Infinity Biologix

Interpath Laboratory

Jefferson Healthcare

Kaiser Permanente Washington Health Research Institute

Labcorp

Laboratories Northwest

Laboratory Corporation of America

Legacy Laboratory

Magnolia Diagnostics, LLC

Mann-Grandstaff VA Medical Center

Mason General Hospital Laboratory

Mid Valley Hospital

Molecular Testing Labs

MultiCare

Avero Diagnostics

OHSU Lab Services Molecular Microbiology Lab

Olympic Medical Center

Overlake Hospital

PeaceHealth

Polyclinic

Premier Medical Laboratory

Providence Medical Group

Public Health Seattle-King County Laboratory

Quest Diagnostics Incorporated

Samaritan Hospital Lab

Seattle & King County Public Health Lab

Seattle Children's Hospital

Seattle Flu Study

Skagit Valley Hospital Laboratory

St. Francis Hospital

St. Joseph Medical Center Microbiology

St. Michael Medical Center Laboratory

Swedish Medical Center

Tacoma General Hospital

The Vancouver Clinic

Tomorrow's Health, LLC

TridentCare Laboratory

TridentCare Laboratory

University of Washington Virology Lab

Virginia Mason Franciscan Health Microbiology

Washington State Department of Health Public Health Laboratories

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The following labs have reported sequencing data that is included in this report:

Aegis Laboratory

Altius Institute for Biomedical Research

Atlas Genomics

Boise VA Medical Center

Centers for Disease Control and Prevention

Curative

Flow Diagnostics

Fulgent Genetics

Ginkgo Bioworks Clinical Laboratory

Gravity Diagnostics, LLC

Grittman Medical Center

Grubaugh Lab

Helix Laboratories

Idaho Bureau of Laboratories

Infinity Biologix

Institute for Systems Biology

Kaiser Permanente

Laboratory Corporation of America

Montana Public Health Laboratory

Naval Health Research Center

Oregon SARS-CoV-2 Genome Sequencing Center

Oregon State Public Health Laboratory

Providence St. Joseph Health Molecular Genomics Laboratory

Quest Diagnostics

Seattle Flu Study

The Jackson Laboratory

The Lauring Laboratory

United States Arm Medical Research Institute of Infectious Diseases

University of Washington Virology Lab

Washington State Department of Health Public Health Laboratories